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T 1: Gene. 1993 Dec 31;137(2):293-7.

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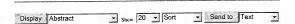
Isolation of the poly(ADP-ribose) polymerase-encoding cDNA from Xenopus laevis: phylogenetic conservation of the functional domains.

Uchida K, Uchida M, Hanai S, Ozawa Y, Ami Y, Kushida S, Miwa M.

Department of Biochemistry, University of Tsukuba, Japan.

The complete nucleotide (nt) sequence of the Xenopus laws poly(ADP-rhose) polymerase (PARP)-encoding cDNA was determined. The putative X, lawsive PARP profit on consists of 1008 amino acids (aa) with a molecular weight of 113 kDa. X, laevis PARP shares 74, 83, 73, 78 and 42% as sequence homology with the human, bovine, mouse, chicken and Drosophila melanogaster PARPs, espectively. Comparison of the PARP as sequences among these species showed conservation of two zinc-finger motifs in the DNA-binding domain, and an NAD-binding motif and a Rossmann fold in the catalytic domain. The first Leu of the putative leutine zipper of D. melanogaster PARP is substituted to Lys in X, laevis PARP. All the Glu residues in the leucine zipper are conserved in these six species.

PMID: 8299962 [PubMed - indexed for MEDLINE]



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